



SEQUENCE LISTING

<110> Cahoon, Rebecca E.
Hitz, William D.
Thorpe, Catherine J.
Tingey, Scott V.

<120> PHYTIC ACID BIOSYNTHETIC ENZYMES

<130> BB1165 US NA

<140> 09/686,522

<141> 2000-10-11

<150> 60/082,960

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<150> PCT/US99/08790

<151> 1999-04-22

<160> 24

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<211> 462

<212> DNA

<213> Oryza sativa

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cggagacgga caaggcctgc gaggacctca tcttcaacca cctccggaag cactaccg 300
accacaagtt catcggcgag gagacgtccg cggggctcgg cgccaccgcg gacctcaccg 360
acgaccgcac ctggatcgtc gacccctcgc atggcaccac caatttcgct catggcttcc 420
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<211> 114

<212> PRT

<213> Oryza sativa

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Ala Gly Glu Ile Ile Arg Lys Gly Phe Tyr Gln Thr Lys Asn Val Glu
20 25 30

His Lys Gly Gln Val Asp Leu Val Thr Glu Thr Asp Lys Ala Cys Glu
35 40 45

Asp Leu Ile Phe Asn His Leu Arg Lys His Tyr Pro Asp His Lys Phe
50 55 60

Ile Gly Glu Glu Thr Ser Ala Gly Leu Gly Ala Thr Ala Asp Leu Thr
65 70 75 80

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Asp Asp Pro Thr Trp Ile Val Asp Pro Leu Asp Gly Thr Thr Asn Phe
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Val His Gly Phe Pro Phe Val Cys Val Ser Ile Gly Leu Thr Val Gly
100 105 110

Lys Ile
114

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<211> 561
<212> DNA
<213> Glycine max

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<223> n = a, c, g or t

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tcctcgcatc tgcggtcgac gcggctcaga aagctggcga gattattcga aaaggcttct 180
accagaccaa aaatgtggaa cacaaaggac aggttgattt ggtcacagaa actgataaag 240
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tgatccctgg atggaactac taacttgtgc atgggttccc tttgtttgtg tccattggc 420
tcacaattgg aaaaatctac aattggtgtt gtatacaatc aatataatga cttttctgga 480
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<210> 4
<211> 168
<212> PRT
<213> Glycine max

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Ala Ala Gln Lys Ala Gly Glu Ile Ile Arg Lys Gly Phe Tyr Gln Thr
20 25 30

Lys Asn Val Glu His Lys Gly Gln Val Asp Leu Val Thr Glu Thr Asp
35 40 45

Lys Ala Cys Glu Glu Leu Ile Phe Asn His Leu Lys Gln Leu Tyr Pro
50 55 60

Thr His Lys Phe Ile Gly Glu Glu Thr Thr Ala Ala Tyr Gly Thr Thr
65 70 75 80

Glu Leu Thr Asp Glu Pro Thr Trp Ile Val Asp Pro Leu Asp Gly Thr
85 90 95

Thr Asn Phe Val His Gly Phe Pro Phe Val Cys Val Ser Ile Gly Leu
100 105 110

Thr Ile Gly Lys Thr Pro Thr Ile Gly Val Val Tyr Asn Pro Ile Ile
115 120 125

Asn Glu Leu Phe Thr Gly Ile His Gly Lys Gly Ala Phe Leu Asn Gly
130 135 140

Asn Pro Ile Lys Val Ser Ser Gln Thr Glu Leu Ile Ser Ser Leu Leu
145 150 155 160

Ala Thr Glu Ala Gly Thr Lys Arg
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<211> 667
<212> DNA
<213> Glycine max

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cagattttgc aataacatct cagcgagtag cagtttcaaa ccctttctaa aaggatgaac 180
ttgtggaaac tcggcgcaaa atgggggtgg aaattttaca ttaaccattg gcaagacctt 240
acaagatagc caacctttgt tagtccgta acctttggcc caaagagttt tttagattcc 300
aagttttacg tagaagttcc aggttaaaaa ggtttttagaa ttttaacttc ctccgggggc 360
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aaaaaactcc ctaaaccatgg gaagaagcac ctccacaggg cagcggttcc caaacctggt 480
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<211> 73
<212> PRT
<213> Glycine max

<220>
<221> UNSURE
<222> (56)
<223> Xaa = any amino acid

<400> 6

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 20 25 30
 Val Val Phe Asp Pro Ser Gly Ala Asp Phe Ala Ile Thr Ser Gln Arg
 35 40 45
 Val Ala Val Ser Asn Pro Phe Xaa Lys Asp Glu Leu Val Glu Thr Arg
 50 55 60
 Arg Lys Met Gly Trp Glu Ile Tyr Asn
 65 70

<210> 7
 <211> 1003
 <212> DNA
 <213> Triticum aestivum

<400> 7
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 agggccaggt ggatttggtg acggagacgg acaaggcatg cgaggatctc atcttcaacc 180
 acctccggat gctctacccg gaccacaagt tcatcggcga ggagacgtct gcagccctcg 240
 gctccaccga tgacctcacc tacgacccca cctggatagt cgacccccctc gatggcacca 300
 ccaacttcgt tcatggcttt ccttttgtgt gcgctctcgat tggcctcacc attgggaaga 360
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 aggtctcttat ggtgacagag gtagggacca aaagagacaa gtccactttg gatgatacaa 540
 ccaacagaat taataagtta ctattcaaga ttagatctat acgtatgtgt ggctcttttg 600
 ctctaaacat gtgtggagtt gcttgtggta ggctagattt gtgttatgag atcgggtttg 660
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 ttgatccgag cggatgatgag tttgatctga tggcgcaaag aatggcagga tcaaattggc 780
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 ttcaagtaga atgaaagaat gtaagatggc cccaccaata agtaattgag ggctactttt 900
 tgtgtagttc tatatgcata ttttgcaaag gtggcggatg taatgacatt ggatatattg 960
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<210> 8
 <211> 267
 <212> PRT
 <213> Triticum aestivum

<400> 8
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 Ala Gly Glu Ile Ile Arg Lys Ser Phe Tyr Leu Ser Lys Lys Val Glu
 20 25 30
 His Lys Gly Gln Val Asp Leu Val Thr Glu Thr Asp Lys Ala Cys Glu
 35 40 45
 Asp Leu Ile Phe Asn His Leu Arg Met Leu Tyr Pro Asp His Lys Phe
 50 55 60
 Ile Gly Glu Glu Thr Ser Ala Ala Leu Gly Ser Thr Asp Asp Leu Thr
 65 70 75 80

Tyr Asp Pro Thr Trp Ile Val Asp Pro Leu Asp Gly Thr Thr Asn Phe
 85 90 95
 Val His Gly Phe Pro Phe Val Cys Val Ser Ile Gly Leu Thr Ile Gly
 100 105 110
 Lys Ile Pro Thr Val Gly Val Val Tyr Asn Pro Ile Met Asn Glu Leu
 115 120 125
 Phe Thr Ala Val Arg Gly Lys Gly Ala Phe Leu Asn Gly Ser Pro Ile
 130 135 140
 Lys Thr Ser Pro Gln Asn Glu Leu Val Lys Ala Leu Met Val Thr Glu
 145 150 155 160
 Val Gly Thr Lys Arg Asp Lys Ser Thr Leu Asp Asp Thr Thr Asn Arg
 165 170 175
 Ile Asn Lys Leu Leu Phe Lys Ile Arg Ser Ile Arg Met Cys Gly Ser
 180 185 190
 Leu Ala Leu Asn Met Cys Gly Val Ala Cys Gly Arg Leu Asp Leu Cys
 195 200 205
 Tyr Glu Ile Gly Phe Gly Gly Pro Trp Asp Val Ala Ala Gly Ala Leu
 210 215 220
 Ile Leu Lys Glu Ala Gly Gly Phe Val Phe Asp Pro Ser Gly Asp Glu
 225 230 235 240
 Phe Asp Leu Met Ala Gln Arg Met Ala Gly Ser Asn Gly His Leu Lys
 245 250 255
 Asp Gln Phe Ile Lys Ala Leu Gly Asp Ala Ser
 260 265

<210> 9
 <211> 1090
 <212> DNA
 <213> Hordeum vulgare

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 gtgcattgat ccttttagatg gaacaacaaa ctttgcacat ggttacccca gcttttctgt 180
 atccattggg gttctttatc gaggcaagcc tgctgctgcc actgtggttg aattttgtgg 240
 tgggcctatg tgctggagca ctogtacaat ttctgcatct tctggcaaag gtgcttattg 300
 taatgggcaa aaaattcatg tcagtccaac agaaaagggtg gaacagtctc ttctggtaac 360
 tgggttttga tatgaacatg atgatgcatg gctcaccaat ataaatttgt tcaaggaatt 420
 tactgatggt agcaggggag tacgaaggct aggtctctgct gctgccgata tgtcccatgt 480
 tgggtctaggc attacagaag cctactggga atatcggcct aagccgtggg acatggctgc 540
 tggcgttctg atagttgaag aagctggttg agtagtgaca cgcattggatg gtggggagtt 600
 tacagtcttt gatcgttctg ttcttgtttc caatggcggtt gttcatgatc agcttttggg 660
 gcggatccgg cctgctactg aagatcctaa gaagaaagga attgatttct ccttgtgggt 720
 taagcctgac aagtacccta ccgacttctg aatcacgctg ctcttcagct acttgttctc 780
 tgtctagcaa aaataaggat gtttttgctg aacaaccatg tacttagact gacaatacat 840
 ttcaagaccc tttcactcaa ccggatcgaa aattaaagcc gaactttaca taaaggagta 900
 gagctcgaat gagcttctca ctggattcct tttgctttga tcgaatgtat caggaagaaa 960
 tgtttgcaaa aggtgttgta tgcattggtc cagcctgttg tacttggaat aatataactg 1020
 ccaattttgt caatcatgga taatagcaag atctctcaag aagacatata ctaaaaaaaaa 1080

aaaaaaaaaa

<210> 10
 <211> 249
 <212> PRT
 <213> Hordeum vulgare

<400> 10
 His Glu Asp Lys Leu Ser Glu Ser Val Ile Leu Glu Val Val Thr Lys
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 Asp Ser Leu Ser Glu Tyr Leu Trp Cys Ile Asp Pro Leu Asp Gly Thr
 35 40 45
 Thr Asn Phe Ala His Gly Tyr Pro Ser Phe Ser Val Ser Ile Gly Val
 50 55 60
 Leu Tyr Arg Gly Lys Pro Ala Ala Ala Thr Val Val Glu Phe Cys Gly
 65 70 75 80
 Gly Pro Met Cys Trp Ser Thr Arg Thr Ile Ser Ala Ser Ser Gly Lys
 85 90 95
 Gly Ala Tyr Cys Asn Gly Gln Lys Ile His Val Ser Pro Thr Glu Lys
 100 105 110
 Val Glu Gln Ser Leu Leu Val Thr Gly Phe Gly Tyr Glu His Asp Asp
 115 120 125
 Ala Trp Leu Thr Asn Ile Asn Leu Phe Lys Glu Phe Thr Asp Val Ser
 130 135 140
 Arg Gly Val Arg Arg Leu Gly Ser Ala Ala Asp Met Ser His Val
 145 150 155 160
 Gly Leu Gly Ile Thr Glu Ala Tyr Trp Glu Tyr Arg Leu Lys Pro Trp
 165 170 175
 Asp Met Ala Ala Gly Val Leu Ile Val Glu Glu Ala Gly Gly Val Val
 180 185 190
 Thr Arg Met Asp Gly Gly Glu Phe Thr Val Phe Asp Arg Ser Val Leu
 195 200 205
 Val Ser Asn Gly Val Val His Asp Gln Leu Leu Glu Arg Ile Arg Pro
 210 215 220
 Ala Thr Glu Asp Leu Lys Lys Lys Gly Ile Asp Phe Ser Leu Trp Phe
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 Lys Pro Asp Lys Tyr Pro Thr Asp Phe
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<210> 11
 <211> 989
 <212> DNA
 <213> Zea mays

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<400> 11
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aaacctgtcc atgaacaagt ccgttggaac caagaacaga gcgatcgaag accgtaaact 420
ctccaccgtc catgcgagtt accaccccac cagcttcctc tactatcagg acgccagcat 480
gcacatccca tggcttaagt cggatttccc agtaagcttc tgtaatacca agtccaatgt 540
gggacatgtc agcagcagca gaccgagcc ttgcgactcc cctgctaatt tcagtaaatt 600
ccttgaacag attcatattg gtcgtccagg catcatcggt ttcatatcca aaacctgtga 660
cgagaagtga ttgttccacc ttgtctgtct gactgacatg aatcctttgt ccaatataat 720
aagctcctcc gccagcaaat ggaaaaattg ttccgggtggt ccaacacata aggccgccac 780
aaaattctca ccacttgaa accacacggg ttttcccagg aaagaacaac taatggcaca 840
ggtaaaccgg ggggtacat tggcaaagtt ccttgtctcc accaaagggt aattgccccca 900
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<210> 12
<211> 136
<212> PRT
<213> Zea mays

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Tyr Tyr Ile Gly Gln Arg Ile His Val Ser Gln Thr Asp Lys Val Glu
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Gln Ser Leu Leu Val Thr Gly Phe Gly Tyr Glu His Asp Asp Ala Trp
          35          40          45

Thr Thr Asn Met Asn Leu Phe Lys Glu Phe Thr Asp Ile Ser Arg Gly
          50          55          60

Val Arg Arg Leu Gly Ser Ala Ala Ala Asp Met Ser His Ile Gly Leu
          65          70          75          80

Gly Ile Thr Glu Ala Tyr Trp Glu Tyr Arg Leu Lys Pro Trp Asp Val
          85          90          95

His Ala Gly Val Leu Ile Val Glu Glu Ala Gly Gly Val Val Thr Arg
          100          105          110

Met Asp Gly Gly Glu Phe Thr Val Phe Asp Arg Ser Val Leu Val Ser
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Asn Gly Leu Val His Gly Gln Val
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<210> 13
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<212> DNA
<213> Zea mays

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<220>
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<222> (442)
<223> n = a, c, g or t

<220>
<221> unsure
<222> (485)
<223> n = a, c, g or t

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cctcgctcc gcaaacccta acccccgctc tcgctcctc cgctccgcg ccgctcgcc 180
cgtgtcgtcc gcggtcttga gcgcgagtg gcgccagccg atgagtacgg ttagggcctc 240
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ccgccagcgg gttgagatca tcgacaaaga ggaccacagt cctgttataa ttgcagatag 420
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ttgngaaga ga 492

<210> 14
<211> 338
<212> PRT
<213> Zea mays

<400> 14
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35 40 45
Gln Pro Met Ser Thr Val Arg Ala Ser Phe Ala Ala Gly Ala Ala Gly
50 55 60
Arg Arg Ala Ala Ala Val Gly Glu Leu Ala Thr Glu Arg Leu Val Glu
65 70 75 80
Val Ala Gln Arg Ala Ala Asp Ala Ala Gly Glu Val Leu Arg Lys Tyr
85 90 95
Phe Arg Gln Arg Val Glu Ile Ile Asp Lys Glu Asp His Ser Pro Val
100 105 110
Thr Ile Ala Asp Arg Glu Ala Glu Glu Ala Met Val Ser Val Ile Leu
115 120 125
Lys Ser Phe Pro Thr His Ala Ile Phe Gly Glu Glu Asn Gly Trp Arg
130 135 140
Cys Ala Glu Asn Ser Ala Asp Phe Val Trp Val Leu Asp Pro Ile Asp
145 150 155 160

Gly Thr Lys Ser Phe Ile Thr Gly Lys Pro Leu Phe Gly Thr Leu Ile
 165 170 175
 Ala Leu Leu His Asn Gly Lys Pro Val Ile Gly Val Ile Asp Gln Pro
 180 185 190
 Ile Leu Arg Glu Arg Trp Ile Gly Val Asp Gly Lys Gln Thr Thr Leu
 195 200 205
 Asn Gly Gln Glu Ile Ser Val Arg Ser Cys Asn Leu Leu Ala Gln Ala
 210 215 220
 Tyr Leu Tyr Thr Thr Ser Pro His Leu Phe Glu Ala Asp Ala Glu Asp
 225 230 235 240
 Ala Phe Ile Arg Val Arg Asn Lys Val Lys Val Pro Leu Tyr Gly Cys
 245 250 255
 Asp Cys Tyr Ala Tyr Ala Leu Leu Ala Ser Gly Phe Val Asp Ile Val
 260 265 270
 Val Glu Ser Gly Leu Lys Pro Tyr Asp Phe Leu Ser Leu Val Pro Val
 275 280 285
 Ile Glu Gly Ala Gly Gly Ser Ile Thr Asp Trp Arg Gly Asp Lys Leu
 290 295 300
 His Trp Pro Val Thr Ala Glu Ser Arg Pro Thr Ser Phe Asn Val Val
 305 310 315 320
 Ala Ala Gly Asp Ala Arg Val His Lys Glu Ala Leu Asp Ala Leu Arg
 325 330 335

Trp Arg

<210> 15
 <211> 593
 <212> DNA
 <213> Oryza sativa

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 acgaagacta ggttctgctg ctgctgacat gtcccacggt gccctaggca ttacagaagc 180
 ctactgggaa taccgactta agccttggga tatggctgct ggtgttctga tagttgaaga 240
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 agatcttaag aagaaaggaa ttgatttctc cttgtgggtt aaacccgaca aataccctac 420
 cgacttttaa gttgaactcc tcaccagag ctattttata ctactagaag aaaagagaaa 480
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<210> 16
 <211> 142
 <212> PRT
 <213> Oryza sativa

<400> 16
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Thr Phe Arg Leu Arg Ala Met Ala Pro His Ser Thr Pro Leu Glu Leu
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 Asn Arg Phe Ala Glu Val Gly Asn Lys Val Ala Asp Ala Ala Gly Glu
 35 40 45
 Val Ile Arg Lys Tyr Phe Arg Lys Asn Phe Asp Val Ile His Lys His
 50 55 60
 Asp Leu Ser Pro Val Thr Ile Ala Asp Gln Ser Ala Glu Glu Ala Met
 65 70 75 80
 Val Ser Ile Ile Leu Asp Asn Phe Pro Ser His Ala Ile Tyr Gly Glu
 85 90 95
 Glu Asn Gly Trp Arg Cys Glu Glu Lys Asn Ala Asp Tyr Val Trp Val
 100 105 110
 Leu Asp Pro Ile Asp Gly Thr Lys Ser Phe Ile Thr Gly Lys Pro Val
 115 120 125
 Phe Gly Thr Leu Val Ala Leu Leu Gln Asn Gly Thr Pro Ile Leu Gly
 130 135 140
 Ile Ile Asp Gln Pro Val Leu Arg Glu Arg Trp Ile Gly Ile Ala Gly
 145 150 155 160
 Lys Arg Thr Ser Leu Asn Gly Gln Glu Ile Ser Thr Arg Thr Cys Ala
 165 170 175
 Asp Leu Ser Gln Ala Tyr Leu Tyr Thr Thr Ser Pro His Leu Phe Asn
 180 185 190
 Gly Asp Ala Glu Glu Ala Phe Ile Arg Val Arg Ser Lys Val Lys Phe
 195 200 205
 Gln Leu Tyr Gly Cys Asp Cys Tyr Ala Tyr Ala Leu Leu Ser Ser Gly
 210 215 220
 Phe Val Asp Leu Val Val Glu Ser Gly Leu Lys Pro Tyr Asp Phe Leu
 225 230 235 240
 Ala Leu Ile Pro Val Ile Glu Gly Ala Gly Gly Val Ile Thr Asp Trp
 245 250 255
 Lys Gly Asp Lys Leu Phe Trp Glu Ala Ser Pro Leu Ser Ile Ala Thr
 260 265 270
 Ser Phe Asn Val Val Ala Ala Gly Asp Lys Gln Ile His Gln Gln Ala
 275 280 285
 Leu Asp Ser Leu Gln Trp Lys
 290 295

<210> 19
 <211> 1418
 <212> DNA
 <213> Triticum aestivum

<400> 19

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catggagcgg ctggtggcgg tggcgagag cgcggcggtat gcggcggggg aggtgctcag 240
gaagtacttc aggcagcgct tcgagatcat cgacaaagag gaccacagtc ccgtcacgat 300
cgctgataga gaagcagaag aagcaatgac ctcagtcata ctgaagagct ttcctactca 360
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ggtccttgac cccatagatg gaacaaagag cttcataact gggaagcctc tttttggtac 480
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caagttgttc acggtgcacc ctttactcaa taatgatcag tggtttcttg ttgtgtgtta 1140
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200
aaaaaaaaaa aaaaaacaaa aaaaaaaata aaaaaaaaaa aaaaacccccg gggggggggc 1260
ggggaccaa tttcccata tttttttttt ttttaccccc ccccgagggg gtttttttta 1320
taaaacttct gaggggggaa aaaccggggg ttaaccaaa taaatcccct tgaacaaaaa 1380
ccccctttcc ccaagggggg taataaaaaa aaggggccg 1418
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<210> 20

<211> 324

<212> PRT

<213> *Triticum aestivum*

<400> 20

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His Glu Thr Lys Pro Ser Leu Pro Tyr His Leu Arg Ser Pro Ser Leu
 1                5                10                15

Leu Ala Thr Phe Ser Ser Ser Ala Ala Gly Arg Ala Cys Gly Ile Ala
      20                25                30

Gly Arg Trp Met Gly Ser Val Arg Ala Ser Pro Ser Glu Ala Gly Gly
      35                40                45

Trp Ala Val Ala Ala Ala Gly Lys Glu Gly Val Asp Met Glu Arg Leu
      50                55                60

Val Ala Val Ala Gln Ser Ala Ala Asp Ala Ala Gly Glu Val Leu Arg
      65                70                75                80

Lys Tyr Phe Arg Gln Arg Phe Glu Ile Ile Asp Lys Glu Asp His Ser
      85                90                95

Pro Val Thr Ile Ala Asp Arg Glu Ala Glu Glu Ala Met Thr Ser Val
      100                105                110

Ile Leu Lys Ser Phe Pro Thr His Ala Val Phe Gly Glu Glu Asn Gly
      115                120                125

Trp Arg Cys Ala Glu Lys Ser Ala Asp Tyr Val Trp Val Leu Asp Pro
      130                135                140

Ile Asp Gly Thr Lys Ser Phe Ile Thr Gly Lys Pro Leu Phe Gly Thr
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	100		105		110										
Thr	Ile	Glu	Lys	Lys	Pro	Thr	Val	Gly	Val	Val	Tyr	Asn	Pro	Ile	Ile
	115						120					125			
Asp	Glu	Leu	Phe	Thr	Gly	Ile	Asp	Gly	Lys	Gly	Ala	Phe	Leu	Asn	Gly
	130					135					140				
Lys	Pro	Ile	Lys	Val	Ser	Ser	Gln	Ser	Glu	Leu	Val	Lys	Ala	Leu	Leu
	145				150					155					160
Ala	Thr	Glu	Ala	Gly	Thr	Asn	Arg	Asp	Lys	Leu	Val	Val	Asp	Ala	Thr
				165					170						175
Thr	Gly	Arg	Ile	Asn	Ser	Leu	Leu	Phe	Lys	Val	Arg	Ser	Leu	Arg	Met
			180					185					190		
Cys	Gly	Ser	Cys	Ala	Leu	Asn	Leu	Cys	Gly	Val	Ala	Cys	Gly	Arg	Leu
		195					200					205			
Asp	Leu	Phe	Tyr	Glu	Leu	Glu	Phe	Gly	Gly	Pro	Trp	Asp	Val	Ala	Gly
	210					215					220				
Gly	Ala	Val	Ile	Val	Lys	Glu	Ala	Gly	Gly	Phe	Val	Phe	Asp	Pro	Ser
	225				230					235					240
Gly	Ser	Glu	Phe	Asp	Leu	Thr	Ala	Arg	Arg	Val	Ala	Ala	Thr	Asn	Ala
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His	Leu	Lys	Asp	Ala	Phe	Ile	Lys	Ala	Leu	Asn	Glu				
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 <212> PRT
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 Trp Leu Glu Ile Ala Thr Glu Ala Val Leu Ala Ala Gly Ala Glu Ile
 20 25 30
 Phe Ser Leu Trp Gly Lys Val Gln Gln Ile Gln Glu Lys Gly Arg Ala
 35 40 45
 Gly Asp Leu Val Thr Glu Ala Asp Arg Gln Ala Glu Ala Ile Ile Leu
 50 55 60
 Glu Ile Ile Lys Arg Arg Cys Pro Asp His Ala Ile Leu Ala Glu Glu
 65 70 75 80
 Ser Gly Gln Leu Gly Gln Val Asp Asn Pro Phe Cys Trp Ala Ile Asp
 85 90 95
 Pro Leu Asp Gly Thr Thr Asn Phe Ala His Ser Tyr Pro Val Ser Cys
 100 105 110
 Val Ser Ile Gly Leu Leu Ile Gln Asp Ile Pro Thr Val Gly Val Val

115 120 125
 Tyr Asn Pro Phe Arg Gln Glu Leu Phe Arg Ala Ala Thr Ser Leu Gly
 130 135 140
 Ala Thr Leu Asn Arg Arg Pro Ile Gln Val Ser Thr Thr Ala Ser Leu
 145 150 155 160
 Asp Lys Ser Leu Leu Val Thr Gly Phe Ala Tyr Asp Arg Val Lys Thr
 165 170 175
 Leu Asp Asn Asn Tyr Pro Glu Phe Cys Tyr Leu Thr His Leu Thr Gln
 180 185 190
 Gly Val Arg Arg Ser Gly Ser Ala Ala Ile Asp Leu Ile Asp Val Ala
 195 200 205
 Cys Gly Arg Leu Asp Gly Tyr Trp Glu Arg Gly Ile Asn Pro Trp Asp
 210 215 220
 Met Ala Ala Gly Ile Val Ile Val Arg Glu Ala Gly Gly Ile Val Ser
 225 230 235 240
 Ala Tyr Asp Cys Ser Pro Leu Asp Leu Ser Thr Gly Arg Ile Leu Ala
 245 250 255
 Thr Asn Gly Lys Ile His Gln Glu Leu Ser Gln Ala Leu Ala Ala Thr
 260 265 270
 Pro Gln Trp Phe Gln Gln Tyr Ala Ala Ala Arg Ala Gln Lys Ile
 275 280 285
 <210> 24
 <211> 267
 <212> PRT
 <213> Synechocystis sp.
 <400> 24
 Met Leu Pro Glu Val Glu Gln Arg Leu Phe Ile Ala Gln Gln Leu Ala
 1 5 10 15
 Ala Val Ser Gly Glu Ile Leu Ile Gln Tyr Phe Arg Arg Ser His Leu
 20 25 30
 Gln Gly Gly Thr Lys Ile Asp Gln Val Ser Ala Ile Val Thr Gln Ala
 35 40 45
 Asp Glu Glu Ala Glu Gln Ala Met Val Asp Leu Ile Gln Ala Gln Phe
 50 55 60
 Pro Gln Asp Gly Val Ile Arg Glu Glu Gly Lys Asn Ile Ala Gly Lys
 65 70 75 80
 Ser Gly Tyr Thr Trp Val Leu Asp Pro Ile Asp Gly Thr Ser Ser Phe
 85 90 95
 Val Arg Gly Leu Pro Ile Phe Ala Thr Leu Ile Gly Leu Val Asp Ala
 100 105 110
 Asp Met Arg Pro Val Leu Gly Ile Ala His Gln Pro Ile Ser Gly Asp

115 120 125
 Arg Trp Gln Gly Val Gln Gly Glu Gln Ser Asn Val Asn Gly Ile Pro
 130 135 140
 Leu Val Asn Pro Tyr Lys Ala Ser Glu Ile Asn Leu Thr Ala Ala Cys
 145 150 155 160
 Ile Val Ser Thr Thr Pro Leu Met Phe Thr Thr Pro Val Gln Gln Gln
 165 170 175
 Lys Met Ala Asp Ile Tyr Arg Gln Cys Gln Arg Thr Ala Phe Gly Gly
 180 185 190
 Asp Cys Phe Asn Tyr Leu Ser Ala Ala Ser Gly Trp Thr Ala Met Pro
 195 200 205
 Leu Val Ile Val Glu Ala Asp Leu Asn Phe Tyr Asp Phe Cys Ala Leu
 210 215 220
 Ile Pro Ile Leu Thr Gly Ala Asn Tyr Cys Phe Thr Asp Trp Gln Gly
 225 230 235 240
 Lys Glu Leu Thr Pro Glu Ser Thr Glu Val Val Ala Ser Pro Asn Pro
 245 250 255
 Lys Leu His Ser Glu Ile Leu Ala Phe Leu Gln
 260 265
